

Open reading frame 1a, Alignment of aminoacid sequence of PRRS virus strain ATCC VR-2332

1 MSGILDRC TC TPNA RVMMAE GQVY CTRCLS ARSLLPLNLQ VSELGV LGLF YRPEEPLRWT
61 LPRA FPTVEC SPAGACWL SA IFPIIARM TSG NLFN QQR MVR VMAEL YRAGQ LTPAVL KALQ
121 VYER GCRWYP IVGP VP GVAV FANSLH VS DK PFP GATHV LT NIPLP QR PKP EDFCP FECAM
181 ATVY DIGH DA VMYVA ER KV S WAPRG GDEV K FEAV PGEL KL IANRL RT SFP PHHTV DMSK F
241 AFTAP GCG WS MRVER QHG CL PADT VPEG NC WWSL FD IL PL EV QNKE IIR HA NQFG YQT KHG
301 VSG KYL QRR L QVN GL RAV TD LNGPIVVQYF SVKESWIRHL KI LA GEPS YSG FED LL RIR VE
361 PNTSPLAD KE EKIFRF GSHK WY GAGK RARK ARSCA TAT VA GR ALSV RETR QAKE HEV AGA
421 NKAEHL KHYS PPAEGNC GWH CISAIAN RMV NSKFETTL PE RV RPDDWAT DEDLVNA IQI
481 LR LPAA LD RN GACTSA KY VL KLEGE HWT VT VTPG MSP SLL PLECV QGCCG HKGG LGSP D A
541 VE VSG FDP AC LD RL AE VM HL PSSA I PA ALA EMSG DSD RSA SPVTTWTVS QFFAR HSG GN
601 HPDQ VRL GKI ISLC QVIEDC CCSQ NKT NRV TPEEV AA KID LYLRGAT NLE ECLAR LEKAR

Fig. 1

661 PPRVIDTSFD WDVVLPGVAA ATQTIKLPQV NQCRALVPVV TQKSLDNNSV PLTAFSLANY
 721 YYRAQGDEVR HRERLTAVLK KLEKVREY GIMPTEPGPRT TLPRGLDEL KDQMEEDLLK
 781 LANAQTTSDM MAWAVEQVDL KTWWKKNYPRW TPPPPPKVQ PRKTKPVKSL PERKPVPAPR
 841 RKVGSDCGSP VSLGGDVPNS WEDLA VSSPF DLPTPPEPAT PSSELVIVSS PQCIFRPATP
 901 LSEPAPIPAP RGTWSRPTVTP LSEPIPVPA P RRKFQQVKRL SAAAIIIPYYQ DEPLDLSASS
 961 QTEYEASPPA PPQSGGVLGV EGHEAEETLS EISDMSCGNIK PASVSSSSSL SSVRITRPKY
 1021 SAQAIIDSGG PCSGHLQEVK ETCLSSVMREA CDATKLDDPA TQEWLSRMWD RVDDMLTWRNT
 1081 SVYQAICLTD GRLKFLPKMI LETPPPYPCF FVMMMPHTPAP SVGAESDLTI GSVATEDVPR
 1141 ILEKIENVGE MANQGPLAFA EDKPVDDQLV NDPRISSRRP DESTSAPSAG TGGAGSFTDL
 1201 PPSDGADADG GGPFRTVKRK AERLFQQLSR QVFDLVSHLP VFVFSRLFYPG GGYSPGDWGF
 1261 AAFTLLCFL CYSYPAFGIA PLLGVFGSS RRVRMGVFGC WLAFAVGLFK PVSDPVGAAAC

Fig. 1a

1321 EFDSEPCRNI LHSFELLKPW DPVRSLLVVG P VGLGLAILGR LLGGARCIWH FLRLIGIVAD
 1381 CILAGAYVLS QGRCKKCMGS CIRTAPEVA ENVEPETRAT RSSLIDLCDR FCAPKGMDPI
 1441 FLATGWRGCW AGRSPIEQPS EKPIAFAQLD EKKITARTVV AQPYDPNQAV KCLRVLQSGG
 1501 RWWLSG-PKS GQQFRCSIPS PFFPTGVKVD PDCRVVVDPD TFTAAALRSGY STTNLVLGVG
 1561 DFAQLNLGIKI RQISKPSGGG PHIMAALHVA CSMALHMLAG IYVTAVGSCG TGNDPWCAN
 1621 PFAVPGYGP GP SLCTSRLCIS QHGLTLPLTA LVAGFGIQEI ALVVLIFVSI GGMAHRLSCK
 1681 ADMLCVLLAI ASYVWWVPLTW LLCVFPWCWR CFSLHPILIL WLVFFLISVN MPSGILAMVL
 1741 LVSLWLLGRY TNVAGLVTYY DIHHYTSGPR GVAALATAAPD GTYLAAVRRA ALTGRTMLFT
 1801 PSQLGSLLEG AFRTRKPSLN TVNVIGSSMG SGGVFTIDGK VKCVTAAHV L TGNSARVSGV
 1861 GENQMLDEFDV KGDFIAIDCP NWQGAAPKTQ FCTDGWTGRA YWLTTSSGVEP GVIGKGFAFC
 1921 FTACGDSGSP VITEAGELVG VHTGSNKQGG GIVTRPSGQF CNVAPIKLE ISEFFAGPKV
 1981 PLGDVKVGSH IIKDISEVPS DLCAALLAKP ELEGGLSTVQ LLCVFFILLWR MMGHAWTPLV

Fig. 1b

2041 AVSFFILNEV LPAVLVRSVF SFGMFVLSQL TPWSAQVLMF RLLTAALNRM RWSLAFFSLG

2101 AVTGFVADLA ATQGHPLQAV MNLSTYAFLP RMNVVTSPVP VITCGVVHLL AIIYLFKYR

2161 GPHHILVGDG VFSAAFFFLRY FAEGKLREGV SQSCGMNHES LTGALAMRLN DEDDFLMKW

2221 TDFKCFVSAS NMRNAAGQFTI EAAYAKALRV ELAQLWQVDK VRGTLAKLEA FADTVAPQLS

2281 PGDIVVALGH TPVGSIFDLK VGSTKHTLQA IETRVIAGSK MTVARVVDPT PTPPPAPVPI

2341 PLPPKVLENG PNAGDEDRL NKKKRRRMEA LGIYVMGGKK YQKFWDKNSG DVFYEEVHN

2401 TDEWECLRGV DPADFDPEKG TLCGHVTIEN KAYHVYTSPS GKKFLVPPVNP ENGRVQWEAA

2461 KLSVEQALGM MNVDGELTAK ELEKLKRIID KLQGLTKEQC LNC*

Fig. 1c

Open reading frame 1b, Alignment of aminoacid sequence of PRRS virus strain ATCC VR-2332

1 LAASDLTRCG RGGLIVVTTETA VKIVKFNHNR FTLGPVNLKV ASEVELKDAV EHNQHPVARP
61 IDGGGVLLRS AVPSLIDVLI SGADASFKLL AHGPGNIGI DGTLWDFESE ATREEEVLSA
121 QIIQACDIRR GDAPEIGLPI KLYPVGRNPE RVKGVLQNTR FGDIPIYKTPS DTGSPVHAAA
181 CLTPNATPVT DGRSVILATTM PPGFEELVYPT IPASVLDYL SRPDCPKQLT EHGCEDDAALK
241 DLISKYDLSIQ GEVLPGVIRL VRKYLFAHVG KCPPVHRPST YPAKNSMAGI NGNRFPPTKDI
301 QSVPFIDVLC AQAVRENWQT VTPCTLRKQY CGKKRKTRTIL GTNNFTALAH RAVLSGVTQG
361 FMKKAENSPF ALGKANKFKEI QTIPVILGRCLE ADLASCDRST PAIVRWEAN LLYELACAE
421 HLPSYVLNCC HDLLVITQSGA VTKRGGLSSG DPITSVSNTI YSLVVIYAQHM VLSYFVKSGHP
481 HGLLFLQDQI KEEDMIKVQP LIVSDDLVL YAESPTMPNY HWWVTEHLNM LGFQTDPKKT
541 AITDSPSFGLG CRIINGQLV PNRDRILAAI AYHMKASNVS EYYASAAAIL MDSCACLEYD
601 PEWEFEELVVG IAQCARKDGY SEPGBTPEFMS MWEKLRSNYE GKRSRVCGYC GAPAPYATA

Fig. 2

661 GLDVCIYHTH FHQHCPVTIW CGHPAGSGSC SECKSPVGKG TSPIDDEVLEQ VPYKPPRTVI
 721 MHVEQGLTPL DPGRYQTRRG LVSVRRGIRG NEVGLPDGDY ASTALLPTCK EIMMVAVASN
 781 VLRSRFLIGP PGAGKTYWLL QQVQDGDVII TPTHQTMILDM IRAIGTCRFN VPAGTTLQFP
 841 VPSRTGPWVR ILAGGWCPGK NSFLDEAAAYC NHLDVLRLLS KTTLTCLGDF KQLHPVGFDS
 901 HCYVFDIMPO TQLKTIWRFG QNICDAIQPD YRDKLMMSMVN TTRVTVYEKP VRYGQVLTPY
Fig. 2a
 961 HRDREDDAIT IDSSQGATED VVTLHLPTKD SLNRQRALVA ITRARRHALFV YDPHREQLQGL
 1021 FDLPAKGTPV NLAVHCDGQL IVLDRNNKEC TVAQALGNGD KFRATDKRVV DSLRAICADL
 1081 EGSSSPLPKV AHNLFYFSP DLTQEFAKLPV ELAPHWPVVS TQNNEKWPDRL LVASLRPIHK
 1141 YSRACIGAGY MVGPSVFLGT PGVVSYYLTK FVKGGQAQVLP ETVESTGRIE VDCREYLLDDR
 1201 EREVAASLPH GFIGDVKGTW VGGCHHVTSR YLPRVLPKES VAVVGSSPG KAAKALCTLT
 1261 DVYLPDLEAY LHPETQSKCW RMMILDFKEVRL LMVWKDKTAY FQLEGRYFTW YQLASYSASYI

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1321 RVPVNSTIVYL DPCMGALCN RRVVGSTHWG ADLAVTPYDY GAKIILSSAY HGEMPPGYKI

1381 LACAEFSLDD PVKXKHTWGF ESDTAYLYEF TGNGEDWEDY NDAFRARQEG KIYRATATS

1441 KFYFPPGPV1 EPTIGLN*

Fig. 2b

Open reading frame 2, Alignment of aminoacid sequence of PRRS virus strain ATCC VR-2332

1 MKWGPCKAFL TKLANFLWML SRSSWCPLLI SLYFWPFCCLA SPPSPVGWWWSF ASDWFAPRYS
61 VRALPFTLSN YRRSYEAFLS QCQVQDIPTWG TKHPLGMLWH HKVSTLIDEM VSRRMYRIME
121 KAGQQAAWKQV VSEATLRSIS SLDVVAHFQH LAAIEAETCK YLASRLPMLH NLRMTGSNVT
181 IVYNSTLNQV FAIFPTPGSR PKLHDFFQQLW IAVHSSIFSS VAASCTLFVV LWLRVPILRT
241 VFGFRWLGAII FLSNSQ*

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Fig. 3

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	10	20	30	40	50	60
VR 2332	ATGTCGGGA	TACTTGATCG	GTGCACGTGT	ACCCCCAATG	CCAGGGTGT	TATGGCGGAG
	70	80	90	100	110	120
VR 2332	GGCCAAGTCT	ACTGCACACG	ATGCCTCAGT	GCACGGTCTC	TCCTTCCCCT	GAACCTCCAA
	130	140	150	160	170	180
VR 2332	GTTTCTGAGC	TCGGGGTGCT	AGGCCTATTG	TACAGGCCCG	AAGAGCCACT	CCGGTGGACG
	190	200	210	220	230	240
VR 2332	TTGCCACGTG	CATTCCCCAC	TGTTGAGTGC	TCCCCCGCCG	GGGCCTGCTG	GCTTTCTGCA
	250	260	270	280	290	300
VR 2332	ATCTTCCAA	TCGCACGAAT	GACCAGTGGG	AACCTGAACT	TCCAACAAAG	AATGGTACGG
	310	320	330	340	350	360
VR 2332	GTCGCAGCTG	AGCTTACAG	AGCCGGCCAG	CTCACCCCTG	CAGTCTGAA	GGCTCTACAA
	370	380	390	400	410	420
VR 2332	GTTTATGAAC	GGGGTTGCCG	CTGGTACCCC	ATTGTTGGAC	CTGTCCCTGG	AGTGGCCGTT
	430	440	450	460	470	480
VR 2332	TTCGCCAATT	CCCTACATGT	GAGTGATAAA	CCTTTCCCGG	GAGCAACTCA	CGTGTGACCC
	490	500	510	520	530	540
VR 2332	AACCTGCCGC	TCCCGCAGAG	ACCCAAGCCT	GAAGACTTTT	GCCCCTTGAA	GTGTGCTATG
	550	560	570	580	590	600
VR 2332	GCTACTGTCT	ATGACATTGG	TCATGACGCC	GTCATGTATG	TGGCCGAAAG	GAAAGTCTCC
	610	620	630	640	650	660
VR 2332	TGGGCCCTC	GTGGCGGGGA	TGAAGTGAAA	TTTGAAGCTG	TCCCCGGGGA	GTTGAAGTTG
	670	680	690	700	710	720
VR 2332	ATTGCGAACCC	GGCTCCGCAC	CTCCTTCCCG	CCCCACCACAA	CAGTGGACAT	GTCTAAGTTG
	730	740	750	760	770	780
VR 2332	GCCTTCACAG	CCCCTGGGTG	TGGTGTCTCT	ATGCGGGTCG	AACGCCAACAA	CGGCTGCCCTT
	790	800	810	820	830	840
VR 2332	CCCGCTGACA	CTGTCCCTGA	AGGCAACTGC	TGGTGGAGCT	TGTTTGACTT	GCTTCCACTG
	850	860	870	880	890	900
VR 2332	GAAGTTTCAGA	ACAAAGAAAT	TCGCCATGCT	AACCAATTG	GCTACCAGAC	CAAGCATGGT
	910	920	930	940	950	960
VR 2332	GTCTCTGGCA	AGTACCTACA	GCGGAGGCTG	CAAGTTAACG	GTCTCCGAGC	AGTAACGTGAC
	970	980	990	1000	1010	1020
VR 2332	CTAAACGGAC	CTATCGTCGT	ACAGTACTTC	<u>TCCGTTAAGG</u>	AGAGTTGGAT	CCGCCATTG
	1030	1040	1050	1060	1070	1080
VR 2332	AAAATGGCGG	GAGAACCCAG	CTACTCTGGG	TTTGAGGACC	TCCTCAGAAT	AAGGGTTGAG
	1090	1100	1110	1120	1130	1140
VR 2332	CCTAACACGT	CGCCATTGGC	TGACAAGGAA	GAAAAAAATTG	TCCGGTTGG	CAGTCACAAG
	1150	1160	1170	1180	1190	1200
VR 2332	TGGTACGGCG	CTGGAAAGAG	AGCAAGAAAA	GCACGCTCTT	GTGCGACTGC	TACAGTCGCT
	1210	1220	1230	1240	1250	1260
VR 2332	GGCCCGCGCTT	TGTCCGTTCG	TGAAACCCGG	CAGGCCAAGG	AGCACCGAGGT	TGCCGGCGCC

Fig. 4

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	1270	1280	1290	1300	1310	1320
VR 2332	AACAAGGCTG	AGCACCTCAA	ACACTACTCC	CCGCCTGCCG	AAGGGAATTG	TGGTTGGCAC
	1330	1340	1350	1360	1370	1380
VR 2332	TGCATTTCCG	CCATCGCCAA	CCGGATGGTG	AATTCCAAAT	TTGAAACCAC	CCTTCCCGAA
	1390	1400	1410	1420	1430	1440
VR 2332	AGAGTGAGAC	CTCCAGATGA	CTGGGCTACT	GACGAGGATC	TTGTGAATGC	CATCCAAATC
	1450	1460	1470	1480	1490	1500
VR 2332	CTCAGACTCC	CTGCGGCCTT	AGACAGGAAC	GGTGCTTGTA	CTAGCGCCAA	GTACGTACTT
	1510	1520	1530	1540	1550	1560
VR 2332	AAGCTGGAAG	GTGAGCATTG	GACTGTCACT	GTGACCCCTG	GGATGTCCCC	TTCTTTGCTC
	1570	1580	1590	1600	1610	1620
VR 2332	CCTCTTGAAT	GTGTTCAAGGG	CTGTTGTGGG	CACAAGGGCG	GTCTTGGTTC	CCCAGATGCA
	1630	1640	1650	1660	1670	1680
VR 2332	GTCGAGGTCT	CCGGATTGTA	CCCTGCCTGC	CTTGACCGGC	TGGCTGAGGT	GATGCACCTG
	1690	1700	1710	1720	1730	1740
VR 2332	CCTAGCAGTG	CTATCCCAGC	CGCTCTGGCC	GAAATGTCTG	GCGATTCCGA	TCGTTGGCCT
	1750	1760	1770	1780	1790	1800
VR 2332	TCTCCGGTCA	CCACCGTGTG	GACTGTTTCG	CAGTTCTTITG	CCCGTCACAG	CGGAGGGAAT
	1810	1820	1830	1840	1850	1860
VR 2332	CACCTGACC	AAGTGCCTT	AGGGAAAATT	ATCAGCCTTT	GTCAGGTGAT	TGAGGACTGC
	1870	1880	1890	1900	1910	1920
VR 2332	TGCTGTTCCC	AGAACAAAAC	CAACCGGGTC	ACCCCGGAGG	AGGTCGCAGC	AAAGATTGAC
	1930	1940	1950	1960	1970	1980
VR 2332	CTGTACCTCC	GTGGTGCAAC	AAATCTTGAA	GAATGCTTGG	CCAGGCTTGA	GAAAGCGCGC
	1990	2000	2010	2020	2030	2040
VR 2332	CCGCCACGCG	TAATCGACAC	CTCCTTTGAT	TGGGATGTTG	TGCTCCCTGG	GGTTGAGGCG
	2050	2060	2070	2080	2090	2100
VR 2332	GCAACCCAGA	CGATCAAGCT	GCCCCAGGTC	AACCAGTGTC	GTGCTCTGGT	CCCTGTTGTG
	2110	2120	2130	2140	2150	2160
VR 2332	ACTCAAAAGT	CCTTGGACAA	CAACTCGGTC	CCCCCTGACCG	CCTTTTCACT	GGCTAACTAC
	2170	2180	2190	2200	2210	2220
VR 2332	TACTACCGTG	CGCAAGGTGA	CGAAGTTCGT	CACCGTGAAA	GACTAACCGC	CGTGCTCTCC
	2230	2240	2250	2260	2270	2280
VR 2332	AAGTTGGAAA	AGGTTGTTCG	AGAAGAATTAT	GGGCTCATGC	CAACCGAGCC	TGGTCCACGG
	2290	2300	2310	2320	2330	2340
VR 2332	CCCACACTGC	CACGCGGGCT	CGACGAACTC	AAAGACCAGA	TGGAGGAGGA	CTTGCTGAAA
	2350	2360	2370	2380	2390	2400
VR 2332	CTGGCTAACG	CCCAGACGAC	TTCGGACATG	ATGGCCTGGG	CAGTCGAGCA	GGTTGACCTA
	2410	2420	2430	2440	2450	2460
VR 2332	AAAACTTGGG	TCAAGAACTA	CCCGCGGTGG	ACACCACAC	CCCCTCCGCC	AAAAGTTCA
	2470	2480	2490	2500	2510	2520
VR 2332	CCTCGAAAAAA	CGAAGCCTGT	CAAGAGCTTG	CCGGAGAGAA	AGCCTGTCCC	CGCCCCGGCG

Fig. 4a

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VR 2332	2530	2540	2550	2560	2570	2580
	AGGAAGGTTG	GGTCCGATTG	TGGCAGCCCG	GTTTCATTAG	GCGGCGATGT	CCCTAACAGT
VR 2332	2590	2600	2610	2620	2630	2640
	TGGGAAGATT	TGGCTGTTAG	TAGCCCCTTT	GATCTCCCGA	CCCCACCTGA	GCCGGCAACA
VR 2332	2650	2660	2670	2680	2690	2700
	CCTTCAAGTG	AGCTGGTGT	TGTGTCCCTCA	CCGCAATGCA	TCTTCAGGCC	GGCGACACCC
VR 2332	2710	2720	2730	2740	2750	2760
	TTGAGTGAGC	CGGCTCCAAT	TCCCGCACCT	CGCGGAAC TG	TGTCTCGACC	GGTGACACCC
VR 2332	2770	2780	2790	2800	2810	2820
	TTGAGTGAGC	CGATCCCTGT	GCCCCGACCG	CGGGCTAAAGT	TTCAGCAGGT	GAAAAGATTG
VR 2332	2830	2840	2850	2860	2870	2880
	AGTCGGCGG	CGGCAATCCC	ACCGTACCAAG	GACGAGCCCC	TGGATTTGTC	TGCTTCCTCA
VR 2332	2890	2900	2910	2920	2930	2940
	CAGACTGAAT	ATGAGGCCTC	TCCCCCAGCA	CCGCCGCAGA	GCGGGGGCGT	TCTGGGAGTA
VR 2332	2950	2960	2970	2980	2990	3000
	GAGGGGCATG	AAGCTGAGGA	AACCCTGAGT	GAAATCTCGG	ACATGTCGGG	TAACATTAAA
VR 2332	3010	3020	3030	3040	3050	3060
	CCTGCGTCCG	TGTCATCAAG	CAGCTCCTTG	TCCAGCGTGA	GAATCACACG	CCCAAAATAC
VR 2332	3070	3080	3090	3100	3110	3120
	TCAGCTCAAG	CCATCATCGA	CTCGGGCGGG	CCCTGCAGTG	GGCATCTCCA	AGAGGTAAAG
VR 2332	3130	3140	3150	3160	3170	3180
	GAAACATGCC	TTAGTGTCA	GCGCGAGGCA	TGTGATGCGA	CTAAGCTTGA	TGACCCCTGCT
VR 2332	3190	3200	3210	3220	3230	3240
	ACGCAGGAAT	GGCTTTCTCG	CATGTGGGAT	CGGGTGGACA	TGCTGACTTG	GCGAACACCG
VR 2332	3250	3260	3270	3280	3290	3300
	TCTGTTTACG	AGGCGATTTG	CACCTTAGAT	GGCAGGTTAA	AGTTCCCTCCC	AAAAATGATA
VR 2332	3310	3320	3330	3340	3350	3360
	CTCGAGACAC	CGCCGCCCTA	TCCGTGTGAG	TTTGTGATGA	TGCCTCACAC	GCCTGCACCT
VR 2332	3370	3380	3390	3400	3410	3420
	TCCGTAGGTG	CGGAGAGCGA	CCTTACCATT	GGCTCAGTTG	CTACTGAAGA	TGTTCCACGC
VR 2332	3430	3440	3450	3460	3470	3480
	ATCCTCGAGA	AAATAGAAAA	TGTCGGCGAG	ATGGCCAACC	AGGGACCCTT	GGCCTTCTCC
VR 2332	3490	3500	3510	3520	3530	3540
	GAGGATAAAC	CGGTAGATGA	CCAACTTGTC	AACGACCCCC	GGATATCGTC	GCGGAGGCCT
VR 2332	3550	3560	3570	3580	3590	3600
	GACCGAGAGCA	CATCAGCTCC	GTCCGCAGGC	ACAGGTGGCG	CCGGCTCTTT	TACCGATTG
VR 2332	3610	3620	3630	3640	3650	3660
	CCGCCTTCAG	ATGGCGCGGA	TGCGGACGGG	GGGGGGCCGT	TTCGGACGGT	AAAAAGAAAA
VR 2332	3670	3680	3690	3700	3710	3720
	GCTGAAAGGC	TCTTGACCA	ACTGAGCCGT	CAGGTTTTG	ACCTCGTCTC	CCATCTCCCT
VR 2332	3730	3740	3750	3760	3770	3780
	GTTTCTTCT	CACGCCCTTT	CTACCCCTGGC	GGTGGTTATT	CTCCGGGTGA	TTGGGGTTTT

Fig. 4b

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	3790	3800	3810	3820	3830	3840
VR 2332	GCAGCTTTA	CTCTATTGTG	CCTCTTTTA	TGTTACAGTT	ACCCAGCCTT	TGGTATTGCT
	3850	3860	3870	3880	3890	3900
VR 2332	CCCCTCTTGG	GTGTGTTTC	TGGGTCTTCT	CGGCAGCGTC	GAATGGGGT	TTTGGCTG
	3910	3920	3930	3940	3950	3960
VR 2332	TGGTTGGCTT	TTGCTGTTGG	TCTGTTCAAG	CCTGTGTCCG	ACCCAGTCGG	CGCTGCTTGT
	3970	3980	3990	4000	4010	4020
VR 2332	GAGTTTGACT	CGCCAGAGTG	TAGAAACATC	CTTCATTCTT	TTGAGCTTCT	CAAACCTTGG
	4030	4040	4050	4060	4070	4080
VR 2332	GACCCTGTTC	GCAGCCTTGT	TGTGGGCC	GTCGGTCTCG	GTCTTGC	TCTTGGCAGG
	4090	4100	4110	4120	4130	4140
VR 2332	TTACTGGCG	GGGCACGCTG	CATCTGGCAC	TTTTGCTTA	GGCTTGGCAT	TGTTGCAGAC
	4150	4160	4170	4180	4190	4200
VR 2332	TGTATCTTGG	CTGGAGCTT	CGTGCTTCT	CAAGGTAGGT	GTAAAAAGTG	CTGGGGATCT
	4210	4220	4230	4240	4250	4260
VR 2332	TGTATAAGAA	CTGCTCCTAA	TGAGGTCGCT	TTAACGTGT	TTCCTTCAC	ACGTGCGACC
	4270	4280	4290	4300	4310	4320
VR 2332	AGGTCGTCAC	TTATCGACCT	GTGCGATCGG	TTTTGTGCGC	CAAAAGGAAT	GGACCCCAT
	4330	4340	4350	4360	4370	4380
VR 2332	TTTCTCGCCA	CTGGGTGGCG	CGGGTGCTGG	GCCGGCCGAA	GCCCCATTGA	GCAACCCTCT
	4390	4400	4410	4420	4430	4440
VR 2332	GAAAAACCCA	TCGCCTTGC	CCAATTGGAT	GAAAAGAAGA	TTACGGCTAG	GACTGTGGTC
	4450	4460	4470	4480	4490	4500
VR 2332	GCCCAGCCTT	ATGACCCCAA	CCAAGCCGTA	AAGTGCTTGC	GGGTATTGCA	GTCGGGTGGG
	4510	4520	4530	4540	4550	4560
VR 2332	CGATGGTGGC	TAAGCGGTCC	CAAAAGTGGT	CAAGGTTTCC	GCTGTTCCAT	TCCGAGCCCC
	4570	4580	4590	4600	4610	4620
VR 2332	TTCTTCCC	CTGGAGTGA	AGTTGACCT	GATTGCAGGG	TCGTGGTTGA	CCCTGACACT
	4630	4640	4650	4660	4670	4680
VR 2332	TTCACTGCAG	CTCTCCGGTC	TGGCTACTCC	ACCACAAACC	TCGTCC	TGTAGGGGAC
	4690	4700	4710	4720	4760	4740
VR 2332	TTTGCCCAGC	TGAATGGATT	AAAAATCAGG	CAAATTCCA	AGCCTTCAGG	GGGAGGCCA
	4750	4760	4770	4780	4790	4800
VR 2332	CATCTCATGG	CTGCCCTGCA	TGTTGCCTGC	TCGATGGCTC	TGCACATGCT	TGCTGGGATT
	4810	4820	4830	4840	4850	4860
VR 2332	TATGTGACTG	CGGTGGGTT	TTGCGGCACC	GGCACCAACG	ACCCGTGGTG	CGCTAACCCG
	4870	4880	4890	4900	4910	4920
VR 2332	TTTGCCTG	CTGGCTACGG	ACCTGGCTCT	CTCTGCACGT	CCAGGTTGTG	CATTCCC
	4930	4940	4950	4960	4970	4980
VR 2332	CACGGCCTTA	CCCTGCCCTT	GACAGCACTT	GTGGCGGGAT	TCGGTATTCA	AGAAATTGCC
	4990	5000	5010	5020	5030	5040
VR 2332	TTGGTCGTTT	TGATTTTGT	TTCCATCGGA	GGCATGGCTC	ATAGGTGAG	CTGTAAGGCT

Fig. 4c

	5050	5060	5070	5080	5090	5100
VR 2332	GACATGCTGT	GTGTTTGCT	TGCAATTGCC	AGCTATGTT	GGGTACCTCT	TACCTGGTTG
	5110	5120	5130	5140	5150	5160
VR 2332	CTTGTGTGT	TTCCTTGCTG	GTTGCGCTGT	TTTCTTTGC	ACCCCTCAC	CATCCTATGG
	5170	5180	5190	5200	5210	5220
VR 2332	TTGGTGTGTTT	TCTTGATTTC	TGTGAATATG	CCTTCAGGAA	TCTTGGCCAT	GGTGTGTTG
	5230	5240	5250	5260	5270	5280
VR 2332	GTTTCTCTTT	GGCTTCTTGG	TCGTTATACT	AATGTTGCTG	GCCTTGTAC	CCCCTACGAC
	5290	5300	5310	5320	5330	5340
VR 2332	ATTCACTCATT	ACACCACTGG	CCCCCGCGGT	GTTGCCGCCT	TGGCTACCAC	ACCAGATGGG
	5350	5360	5370	5380	5390	5400
VR 2332	ACCTACTTGG	CCGCTGTCCG	CCGCGCTGCG	TTGACTGGCC	GCACCATGCT	GTTTACCCCG
	5410	5420	5430	5440	5450	5460
VR 2332	TCCCAGCTTG	GGTCTCTTCT	TGAGGGTGCT	TTCAGAACTC	GAAAGCCCTC	ACTGAACACC
	5470	5480	5490	5500	5510	5520
VR 2332	GTCAATGTGA	TCGGGTCCTC	CATGGGCTCT	GGCGGGGTGT	TTACCATCGA	CGGGAAAGTC
	5530	5540	5550	5560	5570	5580
VR 2332	AAGTGCCTAA	CTGCCGCACA	TGTCCCTAACG	GGCAATTACG	CTCGGGTTTC	CGGGGTCGGC
	5590	5600	5610	5620	5630	5640
VR 2332	TTCAATCAAA	TGCTTGACTT	TGACGTAAAG	GGAGATTTCG	CTATAGCTGA	TTGCCCGAAT
	5650	5660	5670	5680	5690	5700
VR 2332	TGGCAAGGGGG	CTGCCCCCAA	GACCCAATTC	TGCACGGATG	GATGGACTGG	CCGTGCCTAT
	5710	5720	5730	5740	5750	5760
VR 2332	TGGCTAACAT	CCTCTGGCGT	CGAACCCGGC	GTCATTGGAA	AAGGATTTCGC	CTTCTGCTTC
	5770	5780	5790	5800	5810	5820
VR 2332	ACCGCATGTG	GCGATTCCGG	GTCCCCAGTG	ATCACCGAGG	CCGGTGAGCT	TGTCGGCGTT
	5830	5840	5850	5860	5870	5880
VR 2332	CACACGGGAT	CGAATAAACAC	AGGGGGGGGC	ATTGTTACGC	GCCCCTCAGG	CCAGTTTTGT
	5890	5900	5910	5920	5930	5940
VR 2332	AATGTGGCAC	CCATCAAGCT	AAGCGAATT	AGTGAATTCT	TTGCTGGGCC	TAAGGTCCCG
	5950	5960	5970	5980	5990	6000
VR 2332	CTCGGTGATG	TGAAGGTCGG	CAGCCACATA	ATTAAAGACA	TAAGCGAGGT	GCCTTCAGAT
	6010	6020	6030	6040	6050	6060
VR 2332	CTTGTGCTCT	TGCTTGCTGC	CAAACCTGAA	CTGGAAGGAG	GCCTCTCCAC	CGTCCAACCT
	6070	6080	6090	6100	6110	6120
VR 2332	CTTGTGTGT	TTTTCTCCT	GTGGAGAATG	ATGGGACATG	CCTGGACGCC	CTTGGTTGCT
	6130	6140	6150	6160	6170	6180
VR 2332	GTGAGTTTCT	TTATTTGAA	TGAGGTTCTC	CCAGCCGTCC	TGGTCCGGAG	TGTTTTCTCC
	6190	6200	6210	6220	6230	6240
VR 2332	TTTGGAAATGT	TTGTGCTATC	CTGGCTCACG	CCATGGCTTG	CGCAAGTTCT	GATGATCAGG
	6250	6260	6270	6280	6290	6300
VR 2332	CTTCTGACAG	CAGCTCTTAA	CAGGAACAGA	TGGTCACTTG	CCTTTTCAG	CCTCGGGTGC

Fig. 4d

	6310	6320	6330	6340	6350	6360
VR 2332	GTGACCGGTT	TTGTCGCAGA	TCTTGCGGCC	ACTCAGGGC	ATCCGTTGCA	GGCAGTGATG
	6370	6380	6390	6400	6410	6420
VR 2332	AATTTGAGCA	CCTATGCATT	CCTGCCTCGG	ATGATGGTTG	TGACCTCAC	AGTCCCAGTG
	6430	6440	6450	6460	6470	6480
VR 2332	ATCACGTGTG	GTGTCGTGCA	CCTACTTGCC	ATCATTGTTGT	ACTTGTAA	GTACCGTGCG
	6490	6500	6510	6520	6530	6540
VR 2332	CCGCACCATA	TCCTTGTGG	CGATGGAGTG	TTCTCTGCGG	CTTTCTTCTT	GAGATACTTT
	6550	6560	6570	6580	6590	6600
VR 2332	GCCGAGGGAA	AGTTGAGGGAA	AGGGGTGTCG	CAATCCTGCG	GAATGAATCA	TGAGTCTCTG
	6610	6620	6630	6640	6650	6660
VR 2332	ACTGGTGCCC	TCGCTATGAG	ACTCAATGAC	GAGGACTTGG	ATTTCTTAT	GAAATGGACT
	6670	6680	6690	6700	6710	6720
VR 2332	GATTTTAAGT	GCTTTGTTTC	TGCGTCCAAC	ATGAGGAATG	CAGCGGGTCA	ATTTATCGAG
	6730	6740	6750	6760	6770	6780
VR 2332	GCTGCCTATG	CTAAAGCACT	TAGAGTAGAA	CTGGCCCCAGT	TGGTGCAGGT	TGATAAAAGTT
	6790	6800	6810	6820	6830	6840
VR 2332	CGAGGTACTT	TGGCCAAACT	TGAAGCTTT	GCTGATACCG	TGGCACCTCA	ACTCTCGCCC
	6850	6860	6870	6880	6890	6900
VR 2332	GGTGACATTG	TTGTCGCTCT	CGGCCACACG	CCTGTTGGCA	GTATCTCGA	CCTAAAGGTT
	6910	6920	6930	6940	6950	6960
VR 2332	GGTAGCACCA	AGCATACCC	CCAAGCCATT	GAGACCAGAG	TCCTTGCTGG	GTCCAAAATG
	6970	6980	6990	7000	7010	7020
VR 2332	ACCGTGGCGC	GCGTCGTCGA	CCCGACCCCC	ACGCCACAC	CCGCACCCGT	GCCCATCCCC
	7030	7040	7050	7060	7070	7080
VR 2332	CTCCCACCGA	AAGTTCTGGA	GAATGGCCCC	AACGCTTGGG	GGGATGAGGA	CCGTTTGAAT
	7090	7100	7110	7120	7130	7140
VR 2332	AAGAAGAAGA	GGCGCAGGAT	GGAAAGCCCTC	GGCATCTATG	TTATGGCGGG	GAAAAAGTAC
	7150	7160	7170	7180	7190	7200
VR 2332	CAGAAATTGTT	GGGACAAGAA	TTCCGGTGAT	GTGTTTTATG	AGGAGGTCCA	TAATAACACA
	7210	7220	7230	7240	7250	7260
VR 2332	GATGAGTGGG	AGTGTCTCAG	AGTTGGCGAC	CCTGCCACT	TTGACCCCTGA	GAAGGGAAC
	7270	7280	7290	7300	7310	7320
VR 2332	CTGTGTGGAC	ATGTCACCAT	TGAAAACAAG	GCTTACCATG	TTTACACCTC	CCCATCTGGT
	7330	7340	7350	7360	7370	7380
VR 2332	AAGAAGTTCT	TGGTCCCCGT	CAACCCAGAG	AATGGAAGAG	TTCAATGGGA	AGCTGCAAAG
	7390	7400	7410	7420	7430	7440
VR 2332	CTTTCGGTGG	AGCAGGCCCT	AGGTATGATG	AATGTCGACG	GCGAACTGAC	TGCCAAAGAA
	7450	7460	7470	7480	7490	7500
VR 2332	CTGGAGAAC	TGAAAAGAAAT	AATTGACAAA	CTCCAGGGCC	TGACTAAGGA	GCAGTGTGTTA
	7509					
VR 2332	AACTGCTAG					

Fig. 4e

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VR 2332	10	20	30	40	50	60
	CTAGCCGCCA	GCGACTTGAC	CCGCTGTGGT	CGCGGCGGCT	TGGTTGTTAC	TGAAACAGCG
VR 2332	70	80	90	100	110	120
	GTAAAAATAG	TCAAATTCA	CAACCGGACC	TTCACCCCTGG	GACCTGTGAA	TTTAAAAGTG
VR 2332	130	140	150	160	170	180
	GCCAGTGAGG	TTGAGCTAAA	AGACGCGGTT	GAGCACAAACC	AACACCCGGT	TGCGAGACCG
VR 2332	190	200	210	220	230	240
	ATCGATGGTG	GAGTTGTGCT	CCTGCCTTCC	CGGGTTCCCTT	CGCTTATAGA	CGTCTTGATC
VR 2332	250	260	270	280	290	300
	TCCGGTGCTG	ATGCATCTCC	CAAGTTACTT	GCCCATCACG	GGCCGGGAAA	CACTGGGATC
VR 2332	310	320	330	340	350	360
	GATGGCACGC	TCTGGGATT	TGAGTCCGAA	GCCACTAAAG	AGGAAGTCGC	ACTCAGTGCG
VR 2332	370	380	390	400	410	420
	CAAATAATAC	AGGCTTGTGA	CATTAGGCCG	GGCGACGCTC	CTGAAATTGG	TCTCCCTTAC
VR 2332	430	440	450	460	470	480
	AAGCTGTACC	CTGTTAGGGG	TAACCCTGAG	CGGGTGAAAG	GAGTTCTGCA	GAATACAAGG
VR 2332	490	500	510	520	530	540
	TTTGGAGACA	TACCTTACAA	AACCCCCAGT	GACACTGGAA	GCCCAGTGCA	CGCGGCTGCG
VR 2332	550	560	570	580	590	600
	TGCCTTACGC	CCAACGCCAC	TCCGGTGACT	GATGGGCGCT	CCGTCTTGCG	CACGACCATG
VR 2332	610	620	630	640	650	660
	CCCCCCGGGT	TTGAGTTATA	TGTACCGACC	ATACCAGCGT	CTGTCCTTGA	TTACCTTGAC
VR 2332	670	680	690	700	710	720
	TCTAGGCCTG	ACTGCCCTAA	ACAGCTGACA	GAGCACGGCT	GCGAAGATGC	CGCACTGAAA
VR 2332	730	740	750	760	770	780
	GACCTCTCTA	AATATGACTT	GTCCACCCAA	GGCTTTGTTT	TACCTGGAGT	TCTTCGCCTT
VR 2332	790	800	810	820	830	840
	GTGCGGAAAT	ACCTGTTGC	CCATGTAGGT	AAGTGCCCAC	CCGTTCATCG	GCCTTCTACT
VR 2332	850	860	870	880	890	900
	TACCCGTCTA	AGAATTCTAT	GGCTGGAATA	AATGGGAACA	GGTTCCCAAC	CAAGGACATT
VR 2332	910	920	930	940	950	960
	CAGAGCGTCC	CTGAAATCGA	CGTTCTGTGC	GCACAGGCTG	TGCGAGAAAA	CTGGCAAAC
VR 2332	970	980	990	1000	1010	1020
	GTCACCCCTT	GTACTCTTAA	GAAACAGTAT	TGCGGGAAAGA	AGAAGACTAG	GACCATACTC
VR 2332	1030	1040	1050	1060	1070	1080
	GGCACCAATA	ACTTCATCGC	ACTAGCCCAC	CGAGCAGTGT	TGAGTGGTGT	TACCCAGGGC
VR 2332	1090	1100	1110	1120	1130	1140
	TTCATGAAAA	AGGCCTTAA	CTCGCCCATC	GCCCTCGGAA	AGAACAAAGTT	TAAGGAGCTA
VR 2332	1150	1160	1170	1180	1190	1200
	CAGACTCCGG	TCCTGGCAG	GTGCCTTGAA	GCTGATCTCG	CATCCTGCGA	TCGATCCACG
VR 2332	1210	1220	1230	1240	1250	1260
	CCTGCAATTG	TCCGCTGGTT	TGCCGCCAAC	CTTCTTTATG	AACTTGCCCTG	TGCTGAAGAG

Fig. 5

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VR 2332	1270	1280	1290	1300	1310	1320
	CATCTACCGT	CGTACGTGCT	GAACTGCTGC	CACGACTTAC	TGGTCACGCA	GTCCGGCGCA
VR 2332	1330	1340	1350	1360	1370	1380
	GTGACTAAGA	GAGGTGCCCT	GTCGTCTGGC	GACCCGATCA	CCTCTGTGTC	TAACACCATT
VR 2332	1390	1400	1410	1420	1430	1440
	TATAGTTGG	TGATCTATGC	ACAGCATATG	GTGCTTAGTT	ACTTCAAAAG	TGGTCACCCC
VR 2332	1450	1460	1470	1480	1490	1500
	CATGGCCTTC	TGTTCTTACA	AGACCAGCTA	AAGTTTGAGG	ACATGCTCAA	GGTTCAACCC
VR 2332	1510	1520	1530	1540	1550	1560
	CTGATCGTCT	ATTCGGACGA	CCTCGTGCTG	TATGCCGAGT	CTCCCACCAT	GCCAAACTAT
VR 2332	1570	1580	1590	1600	1610	1620
	CACTGGTGGG	TTGAACATCT	GAATTGATG	CTGGGGTTTC	AGACGGACCC	AAAGAAGACA
VR 2332	1630	1640	1650	1660	1670	1680
	GCAATAACAG	ACTCGCCATC	ATTCTAGGC	TGTAGAATAA	TAAATGGGCG	CCAGCTAGTC
VR 2332	1690	1700	1710	1720	1730	1740
	CCCAACCCTG	ACAGGATCCT	CGCGGCCCTC	GCCTATCACA	TGAAGGGAG	TAATGTTCT
VR 2332	1750	1760	1770	1780	1790	1800
	GAATACTATG	CCTCAGCGGC	TGCAATACTC	ATGGACAGCT	TGCTTGT	GGAGTATGAT
VR 2332	1810	1820	1830	1840	1850	1860
	CCTGAATGGT	TTGAAGAACT	TGTAGTTGGA	ATAGCGCAGT	GCGCCCGCAA	GGACGGCTAC
VR 2332	1870	1880	1890	1900	1910	1920
	AGCTTCCCCG	GCACGCCGTT	CTTCATGTCC	ATGTGGAAA	AACTCAGGTC	CAATTATGAG
VR 2332	1930	1940	1950	1960	1970	1980
	GGGAAGAAAGT	CGAGAGTGTG	CGGGTACTGC	GGGGCCCGG	CCCCGTACGC	TACTGCCTGT
VR 2332	1990	2000	2010	2020	2030	2040
	GGCCTCGACG	TCTGCATTTA	CCACACCCAC	TTCCACCAGC	ATTGTCCAGT	CACAATCTGG
VR 2332	2050	2060	2070	2080	2090	2100
	TGTGGCCATC	CAGCGGGTTC	TGGTTCTTGT	AGTGAGTGCA	AATCCCCTGT	AGGGAAAGGC
VR 2332	2110	2120	2130	2140	2150	2160
	ACAAGCCCTT	TAGACGAGGT	GCTGGAACAA	GTCCCGTATA	AGCCCCCACG	GACCGTTATC
VR 2332	2170	2180	2190	2200	2210	2220
	ATGCATGTGG	AGCAGGGTCT	CACCCCCCTT	GATCCAGGTA	GATACAAAC	TCGCCGCGGA
VR 2332	2230	2240	2250	2260	2270	2280
	TTAGTCTCTG	TCAGGGTGG	AATTAGGGGA	AATGAAGTTG	GACTACCAGA	CGGTGATTAT
VR 2332	2290	2300	2310	2320	2330	2340
	GCTAGCACCG	CCTTGCTCCC	TACCTGCAAA	GAGATCAACA	TGGTCGCTGT	CGCTTCCAAT
VR 2332	2350	2360	2370	2380	2390	2400
	GTATTGCGCA	GCAGGTTCAT	CATCGGCCCA	CCCGGTGCTG	GGAAAACATA	CTGGCTCCTT
VR 2332	2410	2420	2430	2440	2450	2460
	CAACAGGTCC	AGGATGGTGA	TGTTATTTAC	ACACCAACTC	ACCAGACCAT	GCTTGACATG
VR 2332	2470	2480	2490	2500	2510	2520
	ATTAGGGCTT	TGGGGACGTG	CCGGTTCAAC	GTCCCGGCAG	GCACAAACGCT	GCAATTCCCC

Fig. 5a

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	2530	2540	2550	2560	2570	2580
VR 2332	GTCCCCTCCC	GCACCGGTCC	GTGGGTTTCGC	ATCCTAGCCG	GCGGTTGGTG	TCCTGGCAAG
	2590	2600	2610	2620	2630	2640
VR 2332	AATTCCCTCC	TAGATGAAGC	AGCGTATTGC	AATCACCTTG	ATGTTTTGAG	GCTTCTTAGT
	2650	2660	2670	2680	2690	2700
VR 2332	AAAACATACCC	TCACCTGTCT	AGGAGACTTC	AAGCAACTCC	ACCCAGTGGG	TTTTGATTCT
	2710	2720	2730	2740	2750	2760
VR 2332	CATTGCTATG	TTTTTGACAT	CATGCCTCAA	ACTCAACTGA	AGACCATCTG	GAGGTTTGGA
	2770	2780	2790	2800	2810	2820
VR 2332	CAGAATATCT	GTGATGCCAT	TCAGCCAGAT	TACAGGGACA	AACTCATGTC	CATGGTCAAC
	2830	2840	2850	2860	2870	2880
VR 2332	ACAAACCCGTG	<u>TGACCTACGT</u>	GGAAAAAACCT	GTCAGGTATG	GGCAGGTCT	CACCCCTAC
	2890	2900	2910	2920	2930	2940
VR 2332	CACAGGGACC	GAGAGGACGA	CGCCATCACT	ATTGACTCCA	GTCAAGGCAC	CACATTGAT
	2950	2960	2970	2980	2990	3000
VR 2332	GTGGTTACAT	TGCATTTGCC	CACTAAAGAT	TCACTCAACA	GGCAAAGAGC	CCTTGTGCT
	3010	3020	3030	3040	3050	3060
VR 2332	ATCACCAAGGG	CAAGACACGC	TATCTTGTG	TATGACCCAC	ACAGGCAGCT	GCAGGGCTTG
	3070	3080	3090	3100	3110	3120
VR 2332	TTTGATCTTC	CTGCAAAAGG	CACGCCCGTC	AACCTCGCAG	TGCACTGCGA	CGGGCAGCTG
	3130	3140	3150	3160	3170	3180
VR 2332	ATCGTGCTGG	ATAGAAATAA	CAAAGAATGC	ACGGTTGCTC	AGGCTCTAGG	CAACGGGGAT
	3190	3200	3210	3220	3230	3240
VR 2332	AAATTTAGGG	CCACAGACAA	GCGTGTTGTA	GATTCTCTCC	GCGCCATTG	TGCTGATCTA
	3250	3260	3270	3280	3290	3300
VR 2332	GAAGGGTCGA	GCTCTCCGCT	CCCCAAGGTC	GCACACAAC	TGGGATTGTTA	TTTCTCACCT
	3310	3320	3330	3340	3350	3360
VR 2332	GATTTAACAC	AGTTTGCTAA	ACTCCCAGTA	GAACTTGCAC	CTCACTGGCC	CGTGGTGTCA
	3370	3380	3390	3400	3410	3420
VR 2332	ACCCAGAACAA	ATGAAAAGTG	GCCGGATCGG	CTGGTTGCCA	GCCTTCGCC	TATCCATAAA
	3430	3440	3450	3460	3470	3480
VR 2332	TACAGCCGCG	CGTGCATCGG	TGCCGGCTAT	ATGGTGGGCC	CTTCGGTGTT	TCTAGGCACT
	3490	3500	3510	3520	3530	3540
VR 2332	CCTGGGGTCG	TGTCATACTA	TCTCACAAA	TTTGTAAAGG	CGGGGGCTCA	AGTGCTTCGG
	3550	3560	3570	3580	3590	3600
VR 2332	GAGACGGTTT	TCAGCACCGG	CCGAATTGAG	GTAGACTGCC	GGGAATATCT	TGATGATCGG
	3610	3620	3630	3640	3650	3660
VR 2332	GA G CGAGAAC	TTGCTGCGTC	CCTCCCACAC	GGTTTCATTG	GCGACGTCAA	AGGCACCTACC
	3670	3680	3690	3700	3710	3720
VR 2332	GTTGGAGGAT	GTCATCATGT	CACCTCCAGA	TACCTCCCGC	GCGTCCTTCC	CAAGGAATCA
	3730	3740	3750	3760	3770	3780
VR 2332	GTTGCGGTAG	TCGGGGTTTC	AAGCCCCGGA	AAAGCCGCGA	AAGCATTGTG	CACACTGACA

Fig. 5b

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VR 2332	3790	3800	3810	3820	3830	3840
	GATGTGTACC	TCCCAGATCT	TGAAGCCTAT	CTCCACCCGG	AGACCCAGTC	CAAGTGCTGG
VR 2332	3850	3860	3870	3880	3890	3900
	AAAATGATGT	TGGACTTCAA	AGAAGTTCGA	CTAATGGTCT	GGAAAGACAA	AACAGCCTAT
VR 2332	3910	3920	3930	3940	3950	3960
	TTCCAACCTG	AAGGTCGCTA	TTTCACCTGG	TATCAGCTTG	CCAGCTATGC	CTCGTACATC
VR 2332	3970	3980	3990	4000	4010	4020
	CGTGTCCCCG	TCAACTCTAC	GGTGTACTTG	GACCCCTGCA	TGGGCCCGC	CCTTGCAAC
VR 2332	4030	4040	4050	4060	4070	4080
	AGGAGAGTCG	TCGGGTCCAC	CCACTGGGGG	GCTGACCTCG	CGGTCACCCC	TTATGATTAC
VR 2332	4090	4100	4110	4120	4130	4140
	GGCGCTAAAA	TTATCCTGTC	TAGCGCGTAC	CATGGTAAA	TGCCCCCGG	ATACAAAATT
VR 2332	4150	4160	4170	4180	4190	4200
	CTGGCGTGC	CGGAGTTCTC	GTTGGATGAC	CCAGTTAAGT	ACAAACATAC	CTGGGGGTTT
VR 2332	4210	4220	4230	4240	4250	4260
	GAATCGGATA	CAGCGTATCT	GTATGAGTTC	ACCGGAAACG	GTGAGGACTG	GGAGGATTAC
VR 2332	4270	4280	4290	4300	4310	4320
	AATGATGCGT	TTCGTGCACG	CCAGGAAGGG	AAAATTATA	AGGCCACTGC	CACCAAGCTTG
VR 2332	4330	4340	4350	4360		4374
	AAGTTTTATT	TTCCCCCGGG	CCCTGTCATT	GAACCAAATT	TAGGCCTGAA	TTGA

Fig. 5c

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VR 2332	10	20	30	40	50	60
	ATGAAATGGG GTCCATGCAA AGCCTTTTG ACAAAATTGG CCAACTTTT GTGGATGCTT					
VR 2332	70	80	90	100	110	120
	TCACGGAGTT CTTGGGTGCC ATTGTTGATA TCATTATATT TTTGGCCATT TTGTTGGCCT					
VR 2332	130	140	150	160	170	180
	TCACCATCGC CGGTTGGCTG GTGGTCTTT GCATCAGATT GGTTTGCTCC GCGATACTCC					
VR 2332	190	200	210	220	230	240
	GTACGCGCCC TGCCATTACAC TCTGAGCAAT TACAGAAGAT CTTATGAGGC CTTTCTTCC					
VR 2332	250	260	270	280	290	300
	CAGTGCCAAG TGGACATTCC CACCTGGGGA ACTAACATC CTTTGGGAT GCTTTGGCAC					
VR 2332	310	320	330	340	350	360
	CATAAGGTGT CAACCCTGAT TGATGAAATG GTGTCGCGTC GAATGTACCG CATCATGGAA					
VR 2332	370	380	390	400	410	420
	AAAGCAGGGC AGGCTGCCTG GAAACAGGTG GTGAGCGAGG CTACGCTGTC TCGCATTAGT					
VR 2332	430	440	450	460	470	480
	AGTTTGGATG TGGTGGCTCA TTTTCAGCAT CTAGCCGCCA TTGAAGCCGA GACCTGTAAA					
VR 2332	490	500	510	520	530	540
	TATTGGCCT CCCGGCTGCC CATGCTACAC AACCTGCGCA TGACAGGGTC AAATGTAACC					
VR 2332	550	560	570	580	590	600
	ATAGTGTATA ATAGCACTTT GAATCAGGTG TTTGCTATT TTCCAACCCC TGGTTCCCGG					
VR 2332	610	620	630	640	650	660
	CCAAAGCTTC ATGATTTCA GCAATGGTTA ATAGCTGTAC ATTCCCTCCAT ATTTTCCTCT					
VR 2332	670	680	690	700	710	720
	GTTGCAGCTT CTTGTACTCT TTTTGGTTGTG CTGTGGTTGC GGGTTCCAAT ACTACGTACT					
VR 2332	730	740	750	760	770	
	GTTTTGGTT TCCGCTGGTT AGGGGCAATT TTTCTTCGA ACTCACAGTG A					

Fig. 6